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SEQUENCE LISTING

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Kudo, Takashi
Iwasaki, Hiroko

<120> NOVEL GALACTOSYLTRANSFERASES, THEIR PEPTIDES, AND
NUCLEIC ACIDS ENCODING THE SAME

<130> 3462.1010-000

<140> PCT/JP03/03846

<141> 2003-03-27

<150> JP 2002-94772

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<150> JP 2002-201344

<151> 2002-07-10

<160> 24

<170> PatentIn Ver. 2.0

<210> 1

<211> 1471

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (105)..(1058)

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cggctgcgct ttcctgtccc caagccgttc tagacgcggg aaaa atg ctt tct gaa 116
Met Leu Ser Glu
1

agc agc tcc ttt ttg aag ggt gtg atg ctt gga agc att ttc tgt gct 164
Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser Ile Phe Cys Ala
5 10 15 20

ttg atc act atg cta gga cac att agg att ggt cat gga aat aga atg 212
Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly His Gly Asn Arg Met
25 30 35

cac cac cat gag cat cat cac cta caa gct cct aac aaa gaa gat atc 260
His His His Glu His His His Leu Gln Ala Pro Asn Lys Glu Asp Ile
40 45 50

ttg aaa att tca gag gat gag cgc atg gag ctc agt aag agc ttt cga 308
Leu Lys Ile Ser Glu Asp Glu Arg Met Glu Leu Ser Lys Ser Phe Arg
55 60 65

gta tac tgt att atc ctt gta aaa ccc aaa gat gtg agt ctt tgg gct 356
Val Tyr Cys Ile Ile Leu Val Lys Pro Lys Asp Val Ser Leu Trp Ala
70 75 80

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gca Ala 85	gta Val	aag Lys	gag Glu	act Thr	tgg Trp 90	acc Thr	aaa Lys	cac His	tgt Cys	gac Asp 95	aaa Lys	gca Ala	gag Glu	ttc Phe	ttc Phe 100	404
agt Ser	tct Ser	gaa Glu	aat Asn	gtt Val 105	aaa Lys	gtg Val	ttt Phe	gag Glu	tca Ser 110	att Ile	aat Asn	atg Met	gac Asp	aca Thr 115	aat Asn	452
gac Asp	atg Met	tgg Trp	tta Leu 120	atg Met	atg Met	aga Arg	aaa Lys	gct Ala 125	tac Tyr	aaa Lys	tac Tyr	gcc Ala	ttt Phe 130	gat Asp	aag Lys	500
tat Tyr	aga Arg	gac Asp 135	caa Gln	tac Tyr	aac Asn	tgg Trp	ttc Phe 140	ttc Phe	ctt Leu	gca Ala	cgc Arg	ccc Pro 145	act Thr	acg Thr	ttt Phe	548
gct Ala 150	atc Ile	att Ile	gaa Glu	aac Asn	cta Leu	aag Lys 155	tat Tyr	ttt Phe	ttg Leu	tta Leu	aaa Lys 160	aag Lys	gat Asp	cca Pro	tca Ser	596
cag Gln 165	cct Pro	ttc Phe	tat Tyr	cta Leu	ggc Gly 170	cac His	act Thr	ata Ile	aaa Lys	tct Ser 175	gga Gly	gac Asp	ctt Leu	gaa Glu	tat Tyr 180	644
gtg Val	ggt Gly	atg Met	gaa Glu	gga Gly 185	gga Gly	att Ile	gtc Val	tta Leu	agt Ser 190	gta Val	gaa Glu	tca Ser	atg Met	aaa Lys 195	aga Arg	692
ctt Leu	aac Asn	agc Ser	ctt Leu 200	ctc Leu	aat Asn	atc Ile	cca Pro	gaa Glu 205	aag Lys	tgt Cys	cct Pro	gaa Glu	cag Gln 210	gga Gly	ggg Gly	740
atg Met	att Ile	tgg Trp 215	aag Lys	ata Ile	tct Ser	gaa Glu	gat Asp 220	aaa Lys	cag Gln	cta Leu	gca Ala	gtt Val 225	tgc Cys	ctg Leu	aaa Lys	788
tat Tyr	gct Ala 230	gga Gly	gta Val	ttt Phe	gca Ala	gaa Glu 235	aat Asn	gca Ala	gaa Glu	gat Asp	gct Ala 240	gat Asp	gga Gly	aaa Lys	gat Asp	836
gta Val 245	ttt Phe	aat Asn	acc Thr	aaa Lys	tct Ser 250	gtt Val	ggg Gly	ctt Leu	tct Ser	att Ile 255	aaa Lys	gag Glu	gca Ala	atg Met	act Thr 260	884
tat Tyr	cac His	ccc Pro	aac Asn	cag Gln 265	gta Val	gta Val	gaa Glu	ggc Gly	tgt Cys 270	tgt Cys	tca Ser	gat Asp	atg Met	gct Ala 275	gtt Val	932
act Thr	ttt Phe	aat Asn	gga Gly 280	ctg Leu	act Thr	cca Pro	aat Asn	cag Gln 285	atg Met	cat His	gtg Val	atg Met	atg Met	tat Tyr	ggg Gly	980
gta Val	tac Tyr	cgc Arg 295	ctt Leu	agg Arg	gca Ala	ttt Phe	ggg Gly 300	cat His	att Ile	ttc Phe	aat Asn	gat Asp 305	gca Ala	ttg Leu	gtt Val	1028
ttc Phe	tta Leu 310	cct Pro	cca Pro	aat Asn	ggt Gly	tct Ser 315	gac Asp	aat Asn	gac Asp	tgagaagtg	gtagaaaagcg					1078

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tgaatatgat ctttgtatag gacgtgtggt gtcattatgt gtagtagtaa ctacatatcc 1138
 aatacagctg tatgtttctt tttcttttct aatttggtgg cactgggtata accacacatt 1198
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 tattatatgt gataaattct aaattatgaa cattagaaat ctgtggggca catatttttg 1378
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<211> 318

<212> PRT

<213> Homo sapiens

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 20 25 30
 Gly Asn Arg Met His His His Glu His His His Leu Gln Ala Pro Asn
 35 40 45
 Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg Met Glu Leu Ser
 50 55 60
 Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val Lys Pro Lys Asp Val
 65 70 75 80
 Ser Leu Trp Ala Ala Val Lys Glu Thr Trp Thr Lys His Cys Asp Lys
 85 90 95
 Ala Glu Phe Phe Ser Ser Glu Asn Val Lys Val Phe Glu Ser Ile Asn
 100 105 110
 Met Asp Thr Asn Asp Met Trp Leu Met Met Arg Lys Ala Tyr Lys Tyr
 115 120 125
 Ala Phe Asp Lys Tyr Arg Asp Gln Tyr Asn Trp Phe Phe Leu Ala Arg
 130 135 140
 Pro Thr Thr Phe Ala Ile Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys
 145 150 155 160
 Lys Asp Pro Ser Gln Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly
 165 170 175
 Asp Leu Glu Tyr Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu
 180 185 190
 Ser Met Lys Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro
 195 200 205
 Glu Gln Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala
 210 215 220

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Val Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala
225 230 235 240

Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile Lys
245 250 255

Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys Cys Ser
260 265 270

Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val
275 280 285

Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Ile Phe Asn
290 295 300

Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser Asp Asn Asp
305 310 315

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 3

gaagatctag aatgcaccac catgagcatc

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<210> 4

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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ataagaatgc ggccgctcag tcattgtcag aaccatttg

39

<210> 5

<211> 67

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 5

ggggacaagt ttgtacaaaa aagcaggctt agaaggagat agaaccatgc tttctgaaag 60
cagctcc

67

<210> 6

<211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 6
ggggaccact ttgtacaaga aagctggggtc tcaatcattg tcagaaccat

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<210> 7
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Peptide Sequence

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Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro
1 5 10 15

Ser Pro Ser

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 8
gtttgcctga aatatgctgg agtat

25

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 9
caacagcctt ctactacctg gttg

24

<210> 10
<211> 35
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Probe Sequence

<400> 10
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<210> 11
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 11
agaaatacac tttcgggaa 19

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 12
tgcagtgcta gacatattac 20

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 13
gctttcctgt cccaagccg ttc 23

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 14
gccccacaga tttctaattgt tc 22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 15
gtaatcagat tccattggaa gc 22

<210> 16
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 16
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tgggacatc 69

<210> 17
<211> 56
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 17
ggggaccact ttgtacaaga aagctgggtc tcagtcattt tctgaaccaa ctggag 56

<210> 18
<211> 948
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(948)

<400> 18
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1 5 10 15
agc att tcc tgg gtt ttg ata act atg ttt ggc caa att cac att cga 96
Ser Ile Ser Trp Val Leu Ile Thr Met Phe Gly Gln Ile His Ile Arg
20 25 30
cac aga ggt caa act caa gac cac gag cac cat cac ctt cgt cca cct 144
His Arg Gly Gln Thr Gln Asp His Glu His His His Leu Arg Pro Pro
35 40 45
aac agg aac gat ttc tta aac act tca aaa gtg ata ctc ttg gag ctc 192
Asn Arg Asn Asp Phe Leu Asn Thr Ser Lys Val Ile Leu Leu Glu Leu
50 55 60

agt	aaa	agt	att	cgt	gtt	ttc	tgt	atc	atc	ttt	gga	gaa	tcc	gaa	gat	240
Ser	Lys	Ser	Ile	Arg	Val	Phe	Cys	Ile	Ile	Phe	Gly	Glu	Ser	Glu	Asp	
65					70					75					80	
gag	agt	tac	tgg	gct	gta	ctg	aaa	gag	acc	tgg	acc	aaa	cac	tgt	gac	288
Glu	Ser	Tyr	Trp	Ala	Val	Leu	Lys	Glu	Thr	Trp	Thr	Lys	His	Cys	Asp	
				85					90					95		
aaa	gca	gag	ctc	tac	gat	act	aaa	aat	gat	aat	ttg	ttc	aat	ata	gaa	336
Lys	Ala	Glu	Leu	Tyr	Asp	Thr	Lys	Asn	Asp	Asn	Leu	Phe	Asn	Ile	Glu	
			100					105					110			
agt	aat	gac	agg	tgg	gta	cag	atg	agg	acc	gct	tac	aaa	tac	gtc	ttt	384
Ser	Asn	Asp	Arg	Trp	Val	Gln	Met	Arg	Thr	Ala	Tyr	Lys	Tyr	Val	Phe	
		115					120					125				
gaa	aag	tat	ggt	gac	aac	tac	aac	tgg	ttc	ttc	ctt	gca	ctt	ccc	act	432
Glu	Lys	Tyr	Gly	Asp	Asn	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Leu	Pro	Thr	
	130					135					140					
acg	ttt	gct	gtc	att	gaa	aat	tta	aag	tac	ctt	ttg	ttt	aca	agg	gat	480
Thr	Phe	Ala	Val	Ile	Glu	Asn	Leu	Lys	Tyr	Leu	Leu	Phe	Thr	Arg	Asp	
145					150					155					160	
gca	tcc	cag	ccc	ttc	tat	ctg	ggc	cac	act	gtt	ata	ttt	gga	gac	ctc	528
Ala	Ser	Gln	Pro	Phe	Tyr	Leu	Gly	His	Thr	Val	Ile	Phe	Gly	Asp	Leu	
				165					170					175		
gaa	tac	gtg	act	gtg	gaa	gga	ggg	att	gtc	tta	agc	aga	gag	ttg	atg	576
Glu	Tyr	Val	Thr	Val	Glu	Gly	Gly	Ile	Val	Leu	Ser	Arg	Glu	Leu	Met	
			180					185					190			
aaa	aga	ctt	aac	aga	ctt	ctc	gat	aac	tct	gag	acc	tgt	gca	gat	caa	624
Lys	Arg	Leu	Asn	Arg	Leu	Leu	Asp	Asn	Ser	Glu	Thr	Cys	Ala	Asp	Gln	
		195					200					205				
agt	gtg	att	tgg	aag	tta	tct	gaa	gat	aag	cag	ctg	gca	ata	tgc	ctg	672
Ser	Val	Ile	Trp	Lys	Leu	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Ile	Cys	Leu	
	210					215					220					
aaa	tat	gca	gga	gtt	cat	gca	gaa	aat	gca	gag	gat	tat	gaa	gga	aga	720
Lys	Tyr	Ala	Gly	Val	His	Ala	Glu	Asn	Ala	Glu	Asp	Tyr	Glu	Gly	Arg	
225					230					235					240	
gat	gta	ttt	aat	aca	aaa	cca	atc	gca	cag	ctt	att	gaa	gag	gca	ttg	768
Asp	Val	Phe	Asn	Thr	Lys	Pro	Ile	Ala	Gln	Leu	Ile	Glu	Glu	Ala	Leu	
				245					250					255		
tct	aat	aac	cct	cag	caa	gta	gta	gaa	ggc	tgc	tgt	tca	gat	atg	gct	816
Ser	Asn	Asn	Pro	Gln	Gln	Val	Val	Glu	Gly	Cys	Cys	Ser	Asp	Met	Ala	
			260					265					270			
att	act	ttc	aat	gga	ctg	acc	ccc	caa	aag	atg	gaa	gta	atg	atg	tat	864
Ile	Thr	Phe	Asn	Gly	Leu	Thr	Pro	Gln	Lys	Met	Glu	Val	Met	Met	Tyr	
		275					280					285				
ggc	ctg	tac	cgg	ctc	agg	gca	ttt	gga	cac	tat	ttc	aat	gac	aca	ctc	912
Gly	Leu	Tyr	Arg	Leu	Arg	Ala	Phe	Gly	His	Tyr	Phe	Asn	Asp	Thr	Leu	
	290					295					300					

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gtt ttc ttg cct cca gtt ggt tca gaa aat gac tga
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 305 310 315

<210> 19
 <211> 315
 <212> PRT
 <213> Homo sapiens

<400> 19
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 20 25 30
 His Arg Gly Gln Thr Gln Asp His Glu His His His Leu Arg Pro Pro
 35 40 45
 Asn Arg Asn Asp Phe Leu Asn Thr Ser Lys Val Ile Leu Leu Glu Leu
 50 55 60
 Ser Lys Ser Ile Arg Val Phe Cys Ile Ile Phe Gly Glu Ser Glu Asp
 65 70 75 80
 Glu Ser Tyr Trp Ala Val Leu Lys Glu Thr Trp Thr Lys His Cys Asp
 85 90 95
 Lys Ala Glu Leu Tyr Asp Thr Lys Asn Asp Asn Leu Phe Asn Ile Glu
 100 105 110
 Ser Asn Asp Arg Trp Val Gln Met Arg Thr Ala Tyr Lys Tyr Val Phe
 115 120 125
 Glu Lys Tyr Gly Asp Asn Tyr Asn Trp Phe Phe Leu Ala Leu Pro Thr
 130 135 140
 Thr Phe Ala Val Ile Glu Asn Leu Lys Tyr Leu Leu Phe Thr Arg Asp
 145 150 155 160
 Ala Ser Gln Pro Phe Tyr Leu Gly His Thr Val Ile Phe Gly Asp Leu
 165 170 175
 Glu Tyr Val Thr Val Glu Gly Gly Ile Val Leu Ser Arg Glu Leu Met
 180 185 190
 Lys Arg Leu Asn Arg Leu Leu Asp Asn Ser Glu Thr Cys Ala Asp Gln
 195 200 205
 Ser Val Ile Trp Lys Leu Ser Glu Asp Lys Gln Leu Ala Ile Cys Leu
 210 215 220
 Lys Tyr Ala Gly Val His Ala Glu Asn Ala Glu Asp Tyr Glu Gly Arg
 225 230 235 240
 Asp Val Phe Asn Thr Lys Pro Ile Ala Gln Leu Ile Glu Glu Ala Leu
 245 250 255
 Ser Asn Asn Pro Gln Gln Val Val Glu Gly Cys Cys Ser Asp Met Ala
 260 265 270
 Ile Thr Phe Asn Gly Leu Thr Pro Gln Lys Met Glu Val Met Met Tyr
 275 280 285
 Gly Leu Tyr Arg Leu Arg Ala Phe Gly His Tyr Phe Asn Asp Thr Leu
 290 295 300
 Val Phe Leu Pro Pro Val Gly Ser Glu Asn Asp
 305 310 315

<210> 20
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Artificially
 Synthesized Primer Sequence

<400> 20
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<210> 21
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
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Synthesized Primer Sequence

<400> 21
cggaattctc agtcattttc tgaaccaact g 31

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 22
gcctgaaata tgcaggagtt ca 22

<210> 23
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 23
ggttattaga caatgcctct tcaataag 28

<210> 24
<211> 36
<212> DNA
<213> Artificial Sequence

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Synthesized Probe Sequence

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<222> (1)
<223> Label FAM

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<222> (36)
<223> Label MGB-TAMRA

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